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ECHO

Further evidence of genetic heterogeneity in familial exudative vitreoretinopathy; exclusion of *EVR1*, *EVR3*, and *EVR4* in a large autosomal dominant pedigree

C Toomes, L M Downey, H M Bottomley, H A Mintz-Hittner, C F Inglehearn



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Background/aims: Familial exudative vitreoretinopathy (FEVR) is an inherited blinding condition characterised by abnormal development of the retinal vasculature. The aim of this study was to perform linkage analysis in a large family affected with FEVR to determine whether the mutation involved was in one of the three known autosomal dominant FEVR loci or in another as yet unidentified gene.

Methods: Genomic DNA samples from family members were polymerase chain reaction (PCR) amplified with fluorescently tagged microsatellite markers spanning the *EVR1/EVR4* locus (11q13–14) and the *EVR3* locus (11p12–13). The resulting PCR products were resolved using an automated DNA sequencer and the alleles sized. These data were used to construct haplotypes across each locus and linkage analysis was performed to prove or exclude linkage.

Results: The clinical evaluation in this family suggested features typical of FEVR, with deficient peripheral retinal vascularisation being the common phenotype in all affected individuals. However, linkage analysis proved that this family has a form of FEVR genetically distinct from the *EVR1*, *EVR3* and *EVR4* loci.

Conclusion: The exclusion of linkage in this family to any of the known FEVR loci proves the existence of a fourth locus for autosomal dominant FEVR and shows that this rare disorder is far more heterogeneous than previously thought.

▲ *British Journal of Ophthalmology* 2005;**89**:194–197.